

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/544,180A
Source: IFW16
Date Processed by STIC: 11/20/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 11/20/2006

PATENT APPLICATION: US/10/544,180A

TIME: 13:47:31

Input Set : N:\efs\10544180a_efs\14-03_US_ST25.txt

Output Set: N:\CRF4\11202006\J544180A.raw

3 <110> APPLICANT: Mohnen, Debra
 4 Hahn, Michael G.
 5 Kolli, Venkata S.K.
 6 Doong, Ron L.
 7 Sterling, Jason D.
 9 <120> TITLE OF INVENTION: Galacturonosyltransferases, nucleic acids encoding same, and
 uses
 10 therefor
 12 <130> FILE REFERENCE: 14-03
 14 <140> CURRENT APPLICATION NUMBER: US 10/544,180A
 15 <141> CURRENT FILING DATE: 2006-03-08
 17 <150> PRIOR APPLICATION NUMBER: US 60/445,539
 18 <151> PRIOR FILING DATE: 2003-02-06
 20 <150> PRIOR APPLICATION NUMBER: PCT/US04/03545
 21 <151> PRIOR FILING DATE: 2004-02-05
 23 <160> NUMBER OF SEQ ID NOS: 58
 25 <170> SOFTWARE: PatentIn version 3.3
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 2022
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Arabidopsis thaliana
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 35 cgatctgtgc ttgtgcttct catatttttc tgtgtttttg caoctctttg cttctttggt 120
 37 ggccgaggag tgtatatcga ttcctcaaat gattattcaa ttgtttctgt gaagcagaat 180
 39 cttgactgga gagaacgttt agcaatgcaa tctgttagat ctcttttctc gaaagagata 240
 41 ctagatgtta tagcaaccag cacagctgat ttgggtcttc ttagccttga ttcttttaag 300
 43 aaaaacaatt tgtctgcac atggcgggga accggagtag acccctcctt tagacattct 360
 45 gagaatccag caactcctga tgtcaaactc aataacctga atgaaaaacg tgacagcatt 420
 47 tcaaaagata gtatccatca gaaagttgag acacctaca agattcacag aaggcaacta 480
 49 agagagaaaa ggcgtgagat gcgggcaaat gagttagttc agcacaatga tgacacgatt 540
 51 ttgaaactcg aaaatgctgc cattgaacgc tctaagtctg ttgattctgc agtccttggt 600
 53 aaatacagta tttggagaag agaaaatgag aatgacaact ctgattcaaa tatacgcttg 660
 55 atgcgggatc aagtaataat ggctagagtc tatagtggga ttgcaaaatt gaaaaacaag 720
 57 aacgatttgt tacaagaact ccaggcccgga cttaaggaca gccaacgggt tttgggggaa 780
 59 gcaacatctg atgctgatct tcctcggagt gcgcatgaga aactcagagc catgggtcaa 840
 61 gtcttggtta aagctaagat gcagttatat gactgcaagc tggttactgg aaagctgaga 900
 63 gcaatgcttc agactgccga cgaacaagtg aggagcttaa agaagcagag tacttttctg 960
 65 gctcagttag cagcaaaaac cattccaaat cctatccatt gcctatcaat gcgcttgact 1020
 67 atcgattact atcttctgtc tccggagaaa agaaaattcc ctggagtgaa aaacctagaa 1080
 69 aaccctaata tttatcatta tgccctcttt tccgacaatg tattagctgc atcagtagtt 1140
 71 gttaactcaa ccatcatgaa tgccaaggat ccttctaagc atgtttttca ccttgctcacg 1200
 73 gataaactca atttcggagc aatgaacatg tggttcctcc taaaccacc cggaaaggca 1260
 75 accatacatg tggaaaacgt cgatgagttt aagtggctca attcatctta ctgtcctgtc 1320

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77 cttegctcagc ttgaatctgc agcaatgaga gactactatt ttaaagcaga ccatccaact 1380
79 tcaggctctt cgaatctaaa atacagaaac ccaaagtatc tatccatgtt gaatcacttg 1440
81 agattctacc tccctgaggt ttatcccaag ctgaacaaaa tccctcttct ggacgatgac 1500
83 atcattgttc agaaagactt gactccactc tgggaagtta acctgaacgg caaagtcaac 1560
85 ggtgcagtcg aaacctgtgg ggaaagtctc cacagattcg acaagtatct caacttttcg 1620
87 aatcctcaca ttgcgaggaa cttcaatcca aatgcttggt gatgggctta tggaatgaac 1680
89 atgttcgacc taaaggaatg gaagagagaa gacatcactg gtatatacca caagtggcaa 1740
91 aacatgaatg agaacaggac actatggaag ctaggggacat tgccaccagg attaataaca 1800
93 ttctacggat taacacatcc cttaaacaag gcgtggcatg tgctgggact tggatataac 1860
95 ccgagtatcg acaagaagga cattgagaat gcagcagtgg ttcactataa cgggaacatg 1920
97 aaaccatggt tggagttggc aatgtccaaa tateggccgt attggacca gtagatcaag 1980
99 tttgatcacc catatcttcg tcgttgcaac cttcatgaat aa 2022
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103 <211> LENGTH: 673
104 <212> TYPE: PRT
105 <213> ORGANISM: Arabidopsis thaliana
107 <400> SEQUENCE: 2
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113 Gly Gly Gly Ser Arg Ser Val Leu Val Leu Leu Ile Phe Phe Cys Val
114 20 25 30
117 Phe Ala Pro Leu Cys Phe Phe Val Gly Arg Gly Val Tyr Ile Asp Ser
118 35 40 45
121 Ser Asn Asp Tyr Ser Ile Val Ser Val Lys Gln Asn Leu Asp Trp Arg
122 50 55 60
125 Glu Arg Leu Ala Met Gln Ser Val Arg Ser Leu Phe Ser Lys Glu Ile
126 65 70 75 80
129 Leu Asp Val Ile Ala Thr Ser Thr Ala Asp Leu Gly Pro Leu Ser Leu
130 85 90 95
133 Asp Ser Phe Lys Lys Asn Asn Leu Ser Ala Ser Trp Arg Gly Thr Gly
134 100 105 110
137 Val Asp Pro Ser Phe Arg His Ser Glu Asn Pro Ala Thr Pro Asp Val
138 115 120 125
141 Lys Ser Asn Asn Leu Asn Glu Lys Arg Asp Ser Ile Ser Lys Asp Ser
142 130 135 140
145 Ile His Gln Lys Val Glu Thr Pro Thr Lys Ile His Arg Arg Gln Leu
146 145 150 155 160
149 Arg Glu Lys Arg Arg Glu Met Arg Ala Asn Glu Leu Val Gln His Asn
150 165 170 175
153 Asp Asp Thr Ile Leu Lys Leu Glu Asn Ala Ala Ile Glu Arg Ser Lys
154 180 185 190
157 Ser Val Asp Ser Ala Val Leu Gly Lys Tyr Ser Ile Trp Arg Arg Glu
158 195 200 205
161 Asn Glu Asn Asp Asn Ser Asp Ser Asn Ile Arg Leu Met Arg Asp Gln
162 210 215 220
165 Val Ile Met Ala Arg Val Tyr Ser Gly Ile Ala Lys Leu Lys Asn Lys
166 225 230 235 240
169 Asn Asp Leu Leu Gln Glu Leu Gln Ala Arg Leu Lys Asp Ser Gln Arg
170 245 250 255

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Input Set : N:\efs\10544180a_efs\14-03_US_ST25.txt

Output Set: N:\CRF4\11202006\J544180A.raw

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177 Glu Lys Leu Arg Ala Met Gly Gln Val Leu Ala Lys Ala Lys Met Gln
178      275      280      285
181 Leu Tyr Asp Cys Lys Leu Val Thr Gly Lys Leu Arg Ala Met Leu Gln
182      290      295      300
185 Thr Ala Asp Glu Gln Val Arg Ser Leu Lys Lys Gln Ser Thr Phe Leu
186 305      310      315      320
189 Ala Gln Leu Ala Ala Lys Thr Ile Pro Asn Pro Ile His Cys Leu Ser
190      325      330      335
193 Met Arg Leu Thr Ile Asp Tyr Tyr Leu Ser Pro Glu Lys Arg Lys
194      340      345      350
197 Phe Pro Arg Ser Glu Asn Leu Glu Asn Pro Asn Leu Tyr His Tyr Ala
198      355      360      365
201 Leu Phe Ser Asp Asn Val Leu Ala Ala Ser Val Val Val Asn Ser Thr
202      370      375      380
205 Ile Met Asn Ala Lys Asp Pro Ser Lys His Val Phe His Leu Val Thr
206 385      390      395      400
209 Asp Lys Leu Asn Phe Gly Ala Met Asn Met Trp Phe Leu Leu Asn Pro
210      405      410      415
213 Pro Gly Lys Ala Thr Ile His Val Glu Asn Val Asp Glu Phe Lys Trp
214      420      425      430
217 Leu Asn Ser Ser Tyr Cys Pro Val Leu Arg Gln Leu Glu Ser Ala Ala
218      435      440      445
221 Met Arg Glu Tyr Tyr Phe Lys Ala Asp His Pro Thr Ser Gly Ser Ser
222      450      455      460
225 Asn Leu Lys Tyr Arg Asn Pro Lys Tyr Leu Ser Met Leu Asn His Leu
226 465      470      475      480
229 Arg Phe Tyr Leu Pro Glu Val Tyr Pro Lys Leu Asn Lys Ile Leu Phe
230      485      490      495
233 Leu Asp Asp Asp Ile Ile Val Gln Lys Asp Leu Thr Pro Leu Trp Glu
234      500      505      510
237 Val Asn Leu Asn Gly Lys Val Asn Gly Ala Val Glu Thr Cys Gly Glu
238      515      520      525
241 Ser Phe His Arg Phe Asp Lys Tyr Leu Asn Phe Ser Asn Pro His Ile
242      530      535      540
245 Ala Arg Asn Phe Asn Pro Asn Ala Cys Gly Trp Ala Tyr Gly Met Asn
246 545      550      555      560
249 Met Phe Asp Leu Lys Glu Trp Lys Lys Arg Asp Ile Thr Gly Ile Tyr
250      565      570      575
253 His Lys Trp Gln Asn Met Asn Glu Asn Arg Thr Leu Trp Lys Leu Gly
254      580      585      590
257 Thr Leu Pro Pro Gly Leu Ile Thr Phe Tyr Gly Leu Thr His Pro Leu
258      595      600      605
261 Asn Lys Ala Trp His Val Leu Gly Leu Gly Tyr Asn Pro Ser Ile Asp
262      610      615      620
265 Lys Lys Asp Ile Glu Asn Ala Ala Val Val His Tyr Asn Gly Asn Met
266 625      630      635      640
269 Lys Pro Trp Leu Glu Leu Ala Met Ser Lys Tyr Arg Pro Tyr Trp Thr

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Output Set: N:\CRF4\11202006\J544180A.raw

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273 Lys Tyr Ile Lys Phe Asp His Pro Tyr Leu Arg Arg Cys Asn Leu His
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277 Glu
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282 <211> LENGTH: 1860
283 <212> TYPE: DNA
284 <213> ORGANISM: Arabidopsis thaliana
286 <400> SEQUENCE: 3
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291 ctcggtcttc acaatggctt tcaactctct ggatttgtca ctgttcaacc ggcttcttca      180
293 tttgagagct ttaccagaat caatgctact aagcatacac agagagatgt atccgaacgg      240
295 gtcgatgagg ttcttcaaaa aatcaatcca gttcttccca agaaaagcga cataaacgtg      300
297 ggttccagag atgtgaatgc aacaagcggc actgattcta aaaaaagagg attaccagtg      360
299 tccccaaactg ttgttgccaa tccaagccct gcaataaaaa caaaatcgga agcctcatat      420
301 acagggtgttc agaggaaaat agtaagtggg gatgaaactt ggagaacttg tgaagtgaaa      480
303 tatgggagct actgcctctg gagggaggaa aataaggaa caatgaaaga tgccaagggtg      540
305 aagcaaatga aggaacgctt gtttgtgggt agagcatact atcccagtat tgctaaaatg      600
307 ccttctcaaa gcaagttgac tcgggatatg aaacagaata tccaagagtt tgagcgtatt      660
309 cttagtgaag gttctcaaga tgctgacctt ccaccacagg ttgataaaaa gttgcagaag      720
311 atggaagctg taattgcaaa ggcaaatgtt tttccagtcg actgtaacaa tgttgacaag      780
313 aaattgagac agatccttga tttgactgag gatgaagcta gtttccacat gaaacagagt      840
315 gtgttctctt accagcttgc agtacagaca atgcctaaga gtcttcattg cttgtcaatg      900
317 cgactaactg tggaaacatt caagtcagat tcaattgagg atcccattag tgagaaattt      960
319 tcagatccct cattacttca ctttgttatc atctccgata atatactagc atcgtccgtt     1020
321 gtgatcaact caacggttgt acatgcaagg gacagtaaaa actttgtttt ccatgtactg     1080
323 acagacgagc agaattactt tgcaatgaaa caatggttta ttaggaatcc ttgcaaacaa     1140
325 tcaactgttc aagtattgaa cattgaaaaa ctcgagctgg acgattctga tatgaaactg     1200
327 tctttgtctg cggagttccg tgtttccttc cccagtggtg accttttggc gtctcaacag     1260
329 aatagaacac actacttata ccttttctct caatctcact atcttcttcc caaattattt     1320
331 gacaaaattg agaaggttgt gattctggat gatgacgttg tagtccagcg agacttatct     1380
333 cccctttggg accttgatat ggaagggaaa gtgaatggcg ctgttaagtc gtgcaactgt     1440
335 agattgggtc agctaaggag tctcaagaga ggaaattttg ataccaatgc ttgtctctgg     1500
337 atgtctggtt tgaatgtcgt tgatcttgct agatggaggg cattgggtgt ttcagaaacc     1560
339 tatcaaaaat attataaaga gatgagtagt ggagatgagt cgagcgaagc aattgcattg     1620
341 caggcaagct tgctcacatt tcaagaccaa gtatatgctc ttgacgacaa atgggctcta     1680
343 tcagggcttg gttatgacta ctacatcaat gcacaagcca taaaaaacgc agccatattg     1740
345 cactataacg ggaacatgaa gccgtggctt gagctgggaa tcccaaatta caaaaactat     1800
347 tggagaaggc atctgagtcg ggaagatcgg ttcttgagtg actgtaacgt gaatccttga     1860
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351 <211> LENGTH: 619
352 <212> TYPE: PRT
353 <213> ORGANISM: Arabidopsis thaliana
355 <400> SEQUENCE: 4
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361 Arg Trp Lys Val Leu Val Ile Gly Val Leu Val Leu Val Ile Leu Ser
362          20          25          30

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365 Met Leu Val Pro Leu Ala Phe Leu Leu Gly Leu His Asn Gly Phe His
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369 Ser Pro Gly Phe Val Thr Val Gln Pro Ala Ser Ser Phe Glu Ser Phe
370      50      55      60
373 Thr Arg Ile Asn Ala Thr Lys His Thr Gln Arg Asp Val Ser Glu Arg
374 65      70      75      80
377 Val Asp Glu Val Leu Gln Lys Ile Asn Pro Val Leu Pro Lys Lys Ser
378      85      90      95
381 Asp Ile Asn Val Gly Ser Arg Asp Val Asn Ala Thr Ser Gly Thr Asp
382      100     105     110
385 Ser Lys Lys Arg Gly Leu Pro Val Ser Pro Thr Val Val Ala Asn Pro
386      115     120     125
389 Ser Pro Ala Asn Lys Thr Lys Ser Glu Ala Ser Tyr Thr Gly Val Gln
390      130     135     140
393 Arg Lys Ile Val Ser Gly Asp Glu Thr Trp Arg Thr Cys Glu Val Lys
394 145     150     155     160
397 Tyr Gly Ser Tyr Cys Leu Trp Arg Glu Glu Asn Lys Glu Pro Met Lys
398      165     170     175
401 Asp Ala Lys Val Lys Gln Met Lys Asp Gln Leu Phe Val Ala Arg Ala
402      180     185     190
405 Tyr Tyr Pro Ser Ile Ala Lys Met Pro Ser Gln Ser Lys Leu Thr Arg
406      195     200     205
409 Asp Met Lys Gln Asn Ile Gln Glu Phe Glu Arg Ile Leu Ser Glu Ser
410      210     215     220
413 Ser Gln Asp Ala Asp Leu Pro Pro Gln Val Asp Lys Lys Leu Gln Lys
414 225     230     235     240
417 Met Glu Ala Val Ile Ala Lys Ala Lys Ser Phe Pro Val Asp Cys Asn
418      245     250     255
421 Asn Val Asp Lys Lys Leu Arg Gln Ile Leu Asp Leu Thr Glu Asp Glu
422      260     265     270
425 Ala Ser Phe His Met Lys Gln Ser Val Phe Leu Tyr Gln Leu Ala Val
426      275     280     285
429 Gln Thr Met Pro Lys Ser Leu His Cys Leu Ser Met Arg Leu Thr Val
430      290     295     300
433 Glu His Phe Lys Ser Asp Ser Leu Glu Asp Pro Ile Ser Glu Lys Phe
434 305     310     315     320
437 Ser Asp Pro Ser Leu Leu His Phe Val Ile Ile Ser Asp Asn Ile Leu
438      325     330     335
441 Ala Ser Ser Val Val Ile Asn Ser Thr Val Val His Ala Arg Asp Ser
442      340     345     350
445 Lys Asn Phe Val Phe His Val Leu Thr Asp Glu Gln Asn Tyr Phe Ala
446      355     360     365
449 Met Lys Gln Trp Phe Ile Arg Asn Pro Cys Lys Gln Ser Thr Val Gln
450      370     375     380
453 Val Leu Asn Ile Glu Lys Leu Glu Leu Asp Asp Ser Asp Met Lys Leu
454 385     390     395     400
457 Ser Leu Ser Ala Glu Phe Arg Val Ser Phe Pro Ser Gly Asp Leu Leu
458      405     410     415
461 Ala Ser Gln Gln Asn Arg Thr His Tyr Leu Ser Leu Phe Ser Gln Ser

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:51; Xaa Pos. 2,3,4,5,8,9,10
Seq#:52; Xaa Pos. 2,3,4,5,6,8,9,10,11,12,13,15,17,18,19,21,23,24,25,27,28
Seq#:52; Xaa Pos. 29,30,31,32,33
Seq#:53; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14
Seq#:54; Xaa Pos. 2,3,4,5,6,9,10,12,15,16,18,19,20,21,22,23,24,25,26,27,28
Seq#:54; Xaa Pos. 30,32,33
Seq#:55; Xaa Pos. 2,4,5,7,9,10,13,15,16,17,18,19,20,21,22,23,25,26,28,29
Seq#:56; Xaa Pos. 3,4,5,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,26
Seq#:56; Xaa Pos. 27,29,30
Seq#:57; Xaa Pos. 2,4,5,6,7,8,10,11,12
Seq#:58; Xaa Pos. 2,3,4,5,6,7,9,10,11,12,13,14,15,16,17,18,20,21,22,26,27
Seq#:58; Xaa Pos. 28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,46,47
Seq#:58; Xaa Pos. 49,50

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:51,52,53,54,55,56,57,58

VERIFICATION SUMMARY

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L:4754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
L:4774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:0
L:4778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:16
L:4782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:32
L:4802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:0
L:4822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0
L:4826 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:16
L:4830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:32
L:4850 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0
L:4854 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:16
L:4893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
L:4897 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:16
L:4921 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:0
L:4941 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:4945 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:16
L:4949 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:32
L:4953 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:48